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16/9

#2

OIPE

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        RAW SEQUENCE LISTING              DATE: 11/20/2001
        PATENT APPLICATION:  US/09/970,532    TIME: 09:54:16

        Input Set : N:\Crf3\RULE60\09970532.txt
        Output Set: N:\CRF3\11202001\I970532.raw

   4 <110> APPLICANT: Taylor, J. Michael
   5        Kehrli, Jr., Marcus
   6        Lee, Eun-Kyung
   7        Mwangi, Simon
   9 <120> TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
  10        AND METHODS OF USE
  12 <130> FILE REFERENCE: 08411-018001
  14 <140> CURRENT APPLICATION NUMBER: 09/970,532
  15 <141> CURRENT FILING DATE: 2001-10-03
  17 <150> PRIOR APPLICATION NUMBER: 09/513,007
  18 <151> PRIOR FILING DATE: 2000-02-25
  20 <160> NUMBER OF SEQ ID NOS: 8
  22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
  24 <210> SEQ ID NO: 1
  25 <211> LENGTH: 2440
  26 <212> TYPE: DNA
  27 <213> ORGANISM: Bos taurus
  29 <220> FEATURE:
  30 <221> NAME/KEY: CDS
  31 <222> LOCATION: (294)...(1706)
  33 <400> SEQUENCE: 1
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  35 tcctctcagc tcaagttttc tcggagctct ccgggctctg ggccgcaggg ctggccttcc   120
  36 gggtttgagg tcctccggat tgggctgtgt ccccgcccca gtctcaaccc tccactcccc   180
  37 gacccgaggc ccgggctcca ctgggcatac gcgaggaccg tgttgctgtc actgtcgcgg   240
  38 gccgccactg ccccagccct gatgggggat tgagaggcca cagctggccg gac atg      296
  39                                                            Met
  40                                                             1
  42 ggc ctc ccc acc gtg cct ggc ctg ctg ctg cca ctg gtg ctt cca gct   344
  43 Gly Leu Pro Thr Val Pro Gly Leu Leu Leu Pro Leu Val Leu Pro Ala
  44             5                   10                  15
  46 ctg ttg gca gat gtg tac ccc gca ggg gtt cag ggg ctg gtc cct cac   392
  47 Leu Leu Ala Asp Val Tyr Pro Ala Gly Val Gln Gly Leu Val Pro His
  48         20                  25                  30
  50 ccc ggg gac ctg gag aag aga gag agt ccc tgt ccc caa gga aaa tat   440
  51 Pro Gly Asp Leu Glu Lys Arg Glu Ser Pro Cys Pro Gln Gly Lys Tyr
  52     35                  40                  45
  54 aac cac ccg caa aat agc acc att tgc tgc acc aag tgc cac aaa ggt   488
  55 Asn His Pro Gln Asn Ser Thr Ile Cys Cys Thr Lys Cys His Lys Gly
  56  50                  55                  60                  65
  58 acc tat ctg tac aat gac tgt ccg ggt cca ggg cga gac acg gac tgc   536
  59 Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Arg Asp Thr Asp Cys
  60                  70                  75                  80
  62 agg gtg tgt gcc cct ggc acc tac act gcc ttg gag aac cat ctc aga   584
  63 Arg Val Cys Ala Pro Gly Thr Tyr Thr Ala Leu Glu Asn His Leu Arg
  64                  85                  90                  95
  66 cga tgc ctg agc tgc tcc agg tgc cgg gac gaa atg ttc cag gtg gag   632
```

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67 Arg Cys Leu Ser Cys Ser Arg Cys Arg Asp Glu Met Phe Gln Val Glu
68         100             105             110
70 att tcg cct tgt gta gtg gac cgg gac act gtg tgc ggc tgc agg aag      680
71 Ile Ser Pro Cys Val Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys
72     115             120             125
74 aac cag tac cgg gaa tac tgg ggt gaa act ggc ttc cgg tgt ctg aac      728
75 Asn Gln Tyr Arg Glu Tyr Trp Gly Glu Thr Gly Phe Arg Cys Leu Asn
76 130             135             140             145
78 tgc agc ctc tgt ccc aat ggc aca gtg aat atc ccc tgc cag gag aga      776
79 Cys Ser Leu Cys Pro Asn Gly Thr Val Asn Ile Pro Cys Gln Glu Arg
80             150             155             160
82 cag gac acc atc tgc cac tgc cat atg ggc ttc ttt ctt aaa ggc gcc      824
83 Gln Asp Thr Ile Cys His Cys His Met Gly Phe Phe Leu Lys Gly Ala
84             165             170             175
86 aag tgc atc tcc tgt cat gat tgt aag aac aag gag tgc gag aag tta      872
87 Lys Cys Ile Ser Cys His Asp Cys Lys Asn Lys Glu Cys Glu Lys Leu
88         180             185             190
90 tgt cca acc cga cct tca act ggt aaa gac tct cag gac cca ggc act      920
91 Cys Pro Thr Arg Pro Ser Thr Gly Lys Asp Ser Gln Asp Pro Gly Thr
92         195             200             205
94 aca gta cta tta ccc ctg gtg att gtc ttc ggg ctt tgc ctg gca tcc      968
95 Thr Val Leu Leu Pro Leu Val Ile Val Phe Gly Leu Cys Leu Ala Ser
96 210             215             220             225
98 ttc gcc tct gtc gtc tta gca tgt cgc tac cag cgg tgg aag ccc aag      1016
99 Phe Ala Ser Val Val Leu Ala Cys Arg Tyr Gln Arg Trp Lys Pro Lys
100             230             235             240
102 ctc tac tcc atc att tgc ggg cag tcg act ctg gta aaa gag ggg gag     1064
103 Leu Tyr Ser Ile Ile Cys Gly Gln Ser Thr Leu Val Lys Glu Gly Glu
104             245             250             255
106 cca gaa ctc ctg gtc ccg gcc cca ggc ttc aac ccc acc acc acc atc     1112
107 Pro Glu Leu Leu Val Pro Ala Pro Gly Phe Asn Pro Thr Thr Thr Ile
108         260             265             270
110 tgc ttc agc tcc acc cca agt tcc agt cct gtc tcc att ccc cct tac     1160
111 Cys Phe Ser Ser Thr Pro Ser Ser Ser Pro Val Ser Ile Pro Pro Tyr
112     275             280             285
114 atc tcc tgt gac cgg tcc aac ttc gga gcc gtc gca tct ccc tcc agc     1208
115 Ile Ser Cys Asp Arg Ser Asn Phe Gly Ala Val Ala Ser Pro Ser Ser
116 290             295             300             305
118 gag acg gcc ccg ccc cat cta aag gct ggc ccc atc ctc ccg ggg cct     1256
119 Glu Thr Ala Pro Pro His Leu Lys Ala Gly Pro Ile Leu Pro Gly Pro
120             310             315             320
122 ccg gcc tcc acc cac ctc tgt acc ccg ggg cct ccg gcc tcc acc cac     1304
123 Pro Ala Ser Thr His Leu Cys Thr Pro Gly Pro Pro Ala Ser Thr His
124             325             330             335
126 ctc tgt acc ccg ggg cct ccg gcc tcc acc cac ctc tgc acc cca gtt     1352
127 Leu Cys Thr Pro Gly Pro Pro Ala Ser Thr His Leu Cys Thr Pro Val
128         340             345             350
130 cag aag tgg gaa gcc agc gcc ccc agc gcc ccc gat cag ctc gcg gat     1400
131 Gln Lys Trp Glu Ala Ser Ala Pro Ser Ala Pro Asp Gln Leu Ala Asp
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RAW SEQUENCE LISTING   DATE: 11/20/2001
PATENT APPLICATION: US/09/970,532   TIME: 09:54:16

Input Set : N:\Crf3\RULE60\09970532.txt
Output Set: N:\CRF3\11202001\I970532.raw

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132     355                  360                  365
134 gcc gac ccc gcg acc ctg tac gcg gtg gtg gac ggc gtg ccc ccg tcg    1448
135 Ala Asp Pro Ala Thr Leu Tyr Ala Val Val Asp Gly Val Pro Pro Ser
136 370                 375                  380                  385
138 cgc tgg aag gag ttg gtg cgg cgg ctg gga ctg agc gag cac gag atc    1496
139 Arg Trp Lys Glu Leu Val Arg Arg Leu Gly Leu Ser Glu His Glu Ile
140                 390                  395                  400
142 gag cgg ctg gag ctg gag aac ggg cgc cac ctg cgc gag gcg cag tac    1544
143 Glu Arg Leu Glu Leu Glu Asn Gly Arg His Leu Arg Glu Ala Gln Tyr
144                 405                  410                  415
146 agc atg ctg gcg gcc tgg cgg cgg cgc acg ccg cgc cgc gag gcc acg    1592
147 Ser Met Leu Ala Ala Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr
148                 420                  425                  430
150 ctg gag ctg ctg ggc cgc gtg ctc agg gac atg gac ctg ctg ggt tgc    1640
151 Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys
152     435                  440                  445
154 ctg gaa aac ata gag gag gcg ctg ggt ggc gcc gcc cgc ctc gcg tcc    1688
155 Leu Glu Asn Ile Glu Glu Ala Leu Gly Gly Ala Ala Arg Leu Ala Ser
156 450                 455                  460                  465
158 gag ccc cgc ctt ctc tgg tgaagccccg cccctccgac tgcgggcctc          1736
159 Glu Pro Arg Leu Leu Trp
160                 470
162 cccgccctgc agacggctgc ttccttcctg tgccaggcag cccggaagga tctgcgagat  1796
163 gccctgtgga cctcctgttt tgttttgttt ttttctggag aggaagtctt ggaggagcag  1856
164 gcacgatctg gcagccactg acctggtgct actcactcag tgtacatagc ttttctcagc  1916
165 tgcctgagtg tgtgtctgtg tgtagtgtgt gtctgcgtgc agtgcgtgtg tttgtgtctc  1976
166 tgtatgtgcg tctgtgtgat gtggagtgtg tgtactcgtg agagaggccg agtgtgcccg  2036
167 gagcccaagg cagtggttgc gaagatgagg ggcgccctgc cttattgcct gtttttttggg  2096
168 cttggagaac tcagcaaggc gacttgggga acctacgtcg gtccctgagc cggtttcgca  2156
169 gtagataagc catctttgta tccactctgc acatccactc atccactctg tacactaata  2216
170 gaaactttgt tgccctgcct ggaccagctg aactgtcccc aggcagcggg ggagcacaga  2276
171 aaaatggggc ctcccaaggg agctagctgt tcagttcagt tcagtcgctc agtcgtgtcc  2336
172 gactctttgc gaccctgtga atcgcaggga cttctgtaaa tacactaaaa tcttccaatt  2396
173 aaagctctgc cctggaggga ctggttaaaa aaaaaaaaa aaaa                    2440
175 <210> SEQ ID NO: 2
176 <211> LENGTH: 471
177 <212> TYPE: PRT
178 <213> ORGANISM: Bos taurus
180 <400> SEQUENCE: 2
181 Met Gly Leu Pro Thr Val Pro Gly Leu Leu Leu Pro Leu Val Leu Pro
182 1               5                   10                  15
183 Ala Leu Leu Ala Asp Val Tyr Pro Ala Gly Val Gln Gly Leu Val Pro
184                 20                  25                  30
185 His Pro Gly Asp Leu Glu Lys Arg Glu Ser Pro Cys Pro Gln Gly Lys
186                 35                  40                  45
187 Tyr Asn His Pro Gln Asn Ser Thr Ile Cys Cys Thr Lys Cys His Lys
188     50                  55                  60
189 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Arg Asp Thr Asp
190 65                  70                  75                  80
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RAW SEQUENCE LISTING   DATE: 11/20/2001
PATENT APPLICATION: US/09/970,532   TIME: 09:54:17

Input Set : N:\Crf3\RULE60\09970532.txt
Output Set: N:\CRF3\11202001\I970532.raw

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191 Cys Arg Val Cys Ala Pro Gly Thr Tyr Thr Ala Leu Glu Asn His Leu
192               85              90              95
193 Arg Arg Cys Leu Ser Cys Ser Arg Cys Arg Asp Glu Met Phe Gln Val
194             100             105             110
195 Glu Ile Ser Pro Cys Val Val Asp Arg Asp Thr Val Cys Gly Cys Arg
196         115             120             125
197 Lys Asn Gln Tyr Arg Glu Tyr Trp Gly Glu Thr Gly Phe Arg Cys Leu
198         130             135             140
199 Asn Cys Ser Leu Cys Pro Asn Gly Thr Val Asn Ile Pro Cys Gln Glu
200 145             150             155                 160
201 Arg Gln Asp Thr Ile Cys His Cys His Met Gly Phe Phe Leu Lys Gly
202             165             170             175
203 Ala Lys Cys Ile Ser Cys His Asp Cys Lys Asn Lys Glu Cys Glu Lys
204             180             185             190
205 Leu Cys Pro Thr Arg Pro Ser Thr Gly Lys Asp Ser Gln Asp Pro Gly
206         195             200             205
207 Thr Thr Val Leu Leu Pro Leu Val Ile Val Phe Gly Leu Cys Leu Ala
208     210             215             220
209 Ser Phe Ala Ser Val Val Leu Ala Cys Arg Tyr Gln Arg Trp Lys Pro
210 225             230             235                 240
211 Lys Leu Tyr Ser Ile Ile Cys Gly Gln Ser Thr Leu Val Lys Glu Gly
212             245             250             255
213 Glu Pro Glu Leu Leu Val Pro Ala Pro Gly Phe Asn Pro Thr Thr Thr
214         260             265             270
215 Ile Cys Phe Ser Ser Thr Pro Ser Ser Ser Pro Val Ser Ile Pro Pro
216     275             280             285
217 Tyr Ile Ser Cys Asp Arg Ser Asn Phe Gly Ala Val Ala Ser Pro Ser
218     290             295             300
219 Ser Glu Thr Ala Pro Pro His Leu Lys Ala Gly Pro Ile Leu Pro Gly
220 305             310             315                 320
221 Pro Pro Ala Ser Thr His Leu Cys Thr Pro Gly Pro Pro Ala Ser Thr
222             325             330             335
223 His Leu Cys Thr Pro Gly Pro Pro Ala Ser Thr His Leu Cys Thr Pro
224         340             345             350
225 Val Gln Lys Trp Glu Ala Ser Ala Pro Ser Ala Pro Asp Gln Leu Ala
226         355             360             365
227 Asp Ala Asp Pro Ala Thr Leu Tyr Ala Val Val Asp Gly Val Pro Pro
228     370             375             380
229 Ser Arg Trp Lys Glu Leu Val Arg Arg Leu Gly Leu Ser Glu His Glu
230 385             390             395                 400
231 Ile Glu Arg Leu Glu Leu Glu Asn Gly Arg His Leu Arg Glu Ala Gln
232             405             410             415
233 Tyr Ser Met Leu Ala Ala Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
234         420             425             430
235 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
236     435             440             445
237 Cys Leu Glu Asn Ile Glu Glu Ala Leu Gly Gly Ala Ala Arg Leu Ala
238     450             455             460
239 Ser Glu Pro Arg Leu Leu Trp
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240 465                     470
242 <210> SEQ ID NO: 3
243 <211> LENGTH: 543
244 <212> TYPE: DNA
245 <213> ORGANISM: Bos taurus
247 <220> FEATURE:
248 <221> NAME/KEY: CDS
249 <222> LOCATION: (1)...(543)
251 <400> SEQUENCE: 3
252 ctg gtc cct cac ccc ggg gac ctg gag aag aga gag agt ccc tgt ccc        48
253 Leu Val Pro His Pro Gly Asp Leu Glu Lys Arg Glu Ser Pro Cys Pro
254  1               5                  10                  15
256 caa gga aaa tat aac cac ccg caa aat agc acc att tgc tgc acc aag        96
257 Gln Gly Lys Tyr Asn His Pro Gln Asn Ser Thr Ile Cys Cys Thr Lys
258             20                  25                  30
260 tgc cac aaa ggt acc tat ctg tac aat gac tgt ccg ggt cca ggg cga       144
261 Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Arg
262         35                  40                  45
264 gac acg gac tgc agg gtg tgt gcc cct ggc acc tac act gcc ttg gag       192
265 Asp Thr Asp Cys Arg Val Cys Ala Pro Gly Thr Tyr Thr Ala Leu Glu
266         50                  55                  60
268 aac cat ctc aga cga tgc ctg agc tgc tcc agg tgc cgg gac gaa atg       240
269 Asn His Leu Arg Arg Cys Leu Ser Cys Ser Arg Cys Arg Asp Glu Met
270  65                  70                  75                  80
272 ttc cag gtg gag att tcg cct tgt gta gtg gac cgg gac act gtg tgc       288
273 Phe Gln Val Glu Ile Ser Pro Cys Val Val Asp Arg Asp Thr Val Cys
274                 85                  90                  95
276 ggc tgc agg aag aac cag tac cgg gaa tac tgg ggt gaa act ggc ttc       336
277 Gly Cys Arg Lys Asn Gln Tyr Arg Glu Tyr Trp Gly Glu Thr Gly Phe
278             100                 105                 110
280 cgg tgt ctg aac tgc agc ctc tgt ccc aat ggc aca gtg aat atc ccc       384
281 Arg Cys Leu Asn Cys Ser Leu Cys Pro Asn Gly Thr Val Asn Ile Pro
282         115                 120                 125
284 tgc cag gag aga cag gac acc atc tgc cac tgc cat atg ggc ttc ttt       432
285 Cys Gln Glu Arg Gln Asp Thr Ile Cys His Cys His Met Gly Phe Phe
286     130                 135                 140
288 ctt aaa ggc gcc aag tgc atc tcc tgt cat gat tgt aag aac aag gag       480
289 Leu Lys Gly Ala Lys Cys Ile Ser Cys His Asp Cys Lys Asn Lys Glu
290 145                 150                 155                 160
292 tgc gag aag tta tgt cca acc cga cct tca act ggt aaa gac tct cag       528
293 Cys Glu Lys Leu Cys Pro Thr Arg Pro Ser Thr Gly Lys Asp Ser Gln
294             165                 170                 175
296 gac cca ggc act aca                                                   543
297 Asp Pro Gly Thr Thr
298             180
301 <210> SEQ ID NO: 4
302 <211> LENGTH: 181
303 <212> TYPE: PRT
304 <213> ORGANISM: Bos taurus
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VERIFICATION SUMMARY   DATE: 11/20/2001
PATENT APPLICATION: US/09/970,532   TIME: 09:54:18

Input Set : N:\Crf3\RULE60\09970532.txt
Output Set: N:\CRF3\11202001\I970532.raw